

10-791-592

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:37 ; Search time 154 Seconds
(without alignments)
871.200 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1970	100.0	374	2	AAR79165	Aar79165 Human mon
2	1970	100.0	374	4	AAG80107	Aag80107 Human CCR
3	1970	100.0	374	6	ABU09083	Abu09083 Human che
4	1970	100.0	374	7	ADD44861	Add44861 Human Pro
5	1970	100.0	374	7	ADD44865	Add44865 Human Pro
6	1970	100.0	374	7	ADP65146	Adp65146 Human che
7	1970	100.0	374	8	ADO29221	Ado29221 Human GPC
8	1823	92.5	344	5	ABG92881	Abg92881 Class I r
9	1823	92.5	344	6	ABU61655	Abu61655 Human mon

10	1823	92.5	344	7	ADF72129	Adf72129	Human	G-p
11	1823	92.5	344	8	ADP86217	Adp86217	Human	MCP
12	1727.5	87.7	329	4	AAB46859	Aab46859	Human	MCP
13	1727.5	87.7	329	5	ABB81055	Abb81055	Human	MCP
14	1651.5	83.8	360	2	AAR79166	Aar79166	Human	mon
15	1651.5	83.8	360	2	AAW35833	Aaw35833	Human	mon
16	1651.5	83.8	360	4	AAG80108	Aag80108	Human	CCR
17	1651.5	83.8	360	4	AAU07614	Aau07614	Human	wil
18	1651.5	83.8	360	6	ABP97725	Abp97725	Amino	aci
19	1651.5	83.8	360	6	ABP81987	Abp81987	Human	C-C
20	1651.5	83.8	360	8	ADM67225	Adm67225	Human	adi
21	1651.5	83.8	360	8	ADL82831	Adl82831	Human	PRO
22	1650.5	83.8	360	4	AAU07613	Aau07613	Human	CCR
23	1645.5	83.5	360	4	ABB56340	Abb56340	Non-endog	
24	1589.5	80.7	347	7	ADF56627	Adf56627	Partial h	
25	1332.5	67.6	373	8	ADM67224	Adm67224	Murine ad	
26	1332.5	67.6	373	8	ADO29222	Ado29222	Mouse GPC	
27	1332.5	67.6	373	8	ADP74040	Adp74040	Murine CC	
28	1244	63.1	354	8	ADO29228	Ado29228	Mouse GPC	
29	1236	62.7	352	4	AAG79089	Aag79089	Amino aci	
30	1234	62.6	354	2	AAW54037	Aaw54037	Mouse CC-	
31	1230	62.4	354	7	ADD44859	Add44859	Rat Prote	
32	1230	62.4	354	7	ADD44863	Add44863	Rat Prote	
33	1224	62.1	352	2	AAW27407	Aaw27407	Human CCR	
34	1224	62.1	352	2	AAW27123	Aaw27123	Human che	
35	1224	62.1	352	2	AAW27125	Aaw27125	Macaque c	
36	1224	62.1	352	2	AAW23835	Aaw23835	Human CC	
37	1224	62.1	352	2	AAW88232	Aaw88232	HIV-1 co-	
38	1224	62.1	352	4	AAE07048	Aae07048	Human G-p	
39	1224	62.1	352	4	AAG80111	Aag80111	Human CCR	
40	1224	62.1	352	4	AAE04321	Aae04321	Human che	
41	1224	62.1	352	4	AAE07039	Aae07039	Human G-p	
42	1224	62.1	352	4	AAB46858	Aab46858	Human HDG	
43	1224	62.1	352	4	AAB83354	Aab83354	Human CCR	
44	1224	62.1	352	4	AAB82948	Aab82948	Human HIV	
45	1224	62.1	352	5	AAU97152	Aau97152	Human G-p	

ALIGNMENTS

RESULT 1

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX

AC AAR79165;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .48
 FT /label= extracellular
 FT Domain 49. .70
 FT /label= transmembrane
 FT Domain 80. .700
 FT /label= transmembrane
 FT Domain 115. .136
 FT /label= transmembrane
 FT Domain 154. .178
 FT /label= transmembrane
 FT Domain 204. .231
 FT /label= transmembrane
 FT Domain 244. .268
 FT /label= transmembrane
 FT Domain 295. .313
 FT /label= transmembrane
 FT Region 314. .375
 FT /label= carboxyl tail

XX

PN WO9519436-A1.

XX

PD 20-JUL-1995.

XX

PF 11-JAN-1995; 95WO-US000476.

XX

PR 13-JAN-1994; 94US-00182962.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Charo I, Coughlin S;

XX

DR WPI; 1995-263866/34.

DR

N-PSDB; AAQ96297.

XX

PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.

XX

PS Claim 2; Fig 1; 84pp; English.

XX

CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pFROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-

CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

RESULT 2

AAG80107

ID AAG80107 standard; protein; 374 AA.

XX

AC AAG80107;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2a protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX


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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
Qy      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
Qy      361 GRAPEASLQDKEGA 374
      ||||||||||||||
Db      361 GRAPEASLQDKEGA 374

```

RESULT 3

ABU09083

ID ABU09083 standard; protein; 374 AA.

XX

AC ABU09083;

XX

DT 23-JUL-2003 (first entry)

XX

DE Human chemokine receptor-2 (CKR-2) polypeptide.

XX

KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;

KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;

KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;

KW abnormal physiology; abnormal proliferation; degeneration; atrophy;

KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.

XX

OS Homo sapiens.

XX

PN US2003018167-A1.

XX

PD 23-JAN-2003.

XX

PF 03-JAN-2002; 2002US-00039659.

XX

PR 05-JUL-1996; 96US-0021664P.

PR 11-OCT-1996; 96US-0028329P.

PR 04-JUN-1997; 97US-0048593P.

PR 03-JUL-1997; 97US-00887977.

XX

PA (SCHE) SCHERING CORP.

XX

PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;

XX

DR WPI; 2003-416900/39.

XX

PT New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful

PT for treating conditions associated with abnormal physiology or

PT development, including inflammatory conditions (e.g. asthma), and

PT abnormal proliferation.

XX

PS Disclosure; Page 9-10; 54pp; English.

XX

SQ Sequence 374 AA;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA 374	
Db	361	GRAPEASLQDKEGA 374	

XX
 DE Human Protein P41597, SEQ ID NO 10292.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; P41597.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          ||||||||||||
Db    361 GRAPEASLQDKEGA 374
```

RESULT 5

ADD44865

ID ADD44865 standard; protein; 374 AA.

XX

AC ADD44865;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P41597, SEQ ID NO 10296.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX
PF 14-AUG-2002; 2002WO-US025765.

Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	GRAPEASLQDKEGA	374

RESULT 6

ADP65146

ID ADP65146 standard; protein; 374 AA.

XX

AC ADP65146;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C).

XX

KW autoimmune disease; arthritide; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; human.

XX

OS Homo sapiens.

XX

PN WO2003072827-A1.

XX

PD 04-SEP-2003.

XX

PF 31-OCT-2002; 2002WO-US035433.

XX

PR 31-OCT-2001; 2001US-0336220P.

XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX

PI Hirsch R, Thorton SL;

XX

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||

Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
 |||

Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374
 |||

Db 361 GRAPEASLQDKEGA 374

RESULT 7

ADO29221

ID ADO29221 standard; protein; 374 AA.

XX

AC ADO29221;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human GPCR CCR2, SEQ ID NO:322.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.

XX

OS Homo sapiens.

XX

PN WO2004040000-A2.

XX

PD 13-MAY-2004.

XX

PF 09-SEP-2003; 2003WO-US028226.

XX

PR 09-SEP-2002; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX

PA (PRIM-) PRIMAL INC.

XX

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX

Db	121	 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	 GRAPEASLQDKEGA	374

RESULT 8

ABG92881

ID ABG92881 standard; peptide; 344 AA.

XX

AC ABG92881;

XX

DT 19-NOV-2002 (first entry)

XX

DE Class I receptors WSXWS motif.

XX

KW Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX

OS Synthetic.

XX

PN WO200264612-A2.

XX

PD 22-AUG-2002.

XX

PF 08-FEB-2002; 2002WO-US003634.

XX

PR 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Roschke V, Rosen CA, Ruben SM;
 XX
 DR WPI; 2002-643455/69.
 XX
 PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX
 PS Example 17; Page 386; 562pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 CC sequence of the WSXWS motif found in class I receptors
 XX
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 5; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
 |
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
 Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
 |
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
 Qy 138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
 |
 Db 121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
 |
 Db 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317


```

          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
QY      318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKKSIG 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKKSIG 344

```

RESULT 9

ABU61655

ID ABU61655 standard; protein; 344 AA.

XX

AC ABU61655;

XX

DT 08-AUG-2003 (first entry)

XX

DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.

XX

KW Human; G-protein chemokine receptor; receptor; HDGNR10; MCP-1;

KW 7-transmembrane receptor; monocyte chemoattractant protein 1.

XX

OS Homo sapiens.

XX

PN US2003023044-A1.

XX

PD 30-JAN-2003.

XX

PF 03-SEP-2002; 2002US-00232686.

XX

PR 06-JUN-1995; 95US-00466343.

PR 18-NOV-1998; 98US-00195662.

PR 25-JUN-1999; 99US-00339912.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2003-456307/43.

XX

PT Producing an antibody, involves immunizing an animal with a polypeptide

PT or with a polypeptide encoded by the human G-protein chemokine receptor

PT clone in ATCC 97183, and recovering the antibody.

XX

PS Disclosure; Fig 2; 23pp; English.

XX

CC The invention relates to a method of producing an antibody, involving

CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)

CC polypeptide (also referred to as a human 7-transmembrane receptor) and

CC recovering an antibody which binds the polypeptide. The method is useful

CC for producing an antibody which binds specifically to the human G-protein

CC chemokine receptor polypeptide. This sequence represents the monocyte

CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the

CC HDGNR10 polypeptide of the invention

XX

SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.4e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
        |||
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
        |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy     138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
        |||
Db     121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
        |||
Db     181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
        |||
Db     241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy     318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSG 361
        |||
Db     301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSG 344

```

RESULT 10

ADF72129

ID ADF72129 standard; protein; 344 AA.

XX

AC ADF72129;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human G-protein chemokine receptor (CCR5) ligand MCP-1.

XX

KW cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5;

KW cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring;

KW cancer; hyperproliferative disorder; human; HDG NR10; ligand; MCP-1.

XX

OS Homo sapiens.

XX

PN US2003166024-A1.

XX

PD 04-SEP-2003.

XX

PF 01-MAY-2002; 2002US-00135839.

XX

PR 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

PR 09-FEB-2001; 2001US-00779879.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

XX
 AC ADP86217;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human MCP-1 receptor protein.
 XX
 KW G-protein chemokine receptor; HDGNR10; CCR5; haematopoiesis;
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
 KW leukaemia; T-cell mediated autoimmune diseases; parasitic infection;
 KW psoriasis; allergy; anaphylaxis; atherogenesis; malignancy; inflammation;
 KW prostaglandin-independent fever; bone marrow failure; silicosis;
 KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome;
 KW human; MCP-1 receptor ; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US6743594-B1.
 XX
 PD 01-JUN-2004.
 XX
 PF 11-FEB-2000; 2000US-00502784.
 XX
 PR 06-JUN-1995; 95US-00466343.
 PR 18-NOV-1998; 98US-00195662.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 2004-459648/43.
 XX
 PT Screening compounds binding to G-protein chemokine receptor HDGNR10,
 PT involves contacting test compound with polypeptide of HDGRN10, and
 PT observing binding of test compound to polypeptide.
 XX
 PS Disclosure; SEQ ID NO 9; 26pp; English.
 XX
 CC The invention relates to a method for screening compounds which bind the
 CC G-protein chemokine receptor HDGNR10 (CCR5). Compounds identified by the
 CC method of the invention are useful for stimulating haematopoiesis, wound
 CC healing, coagulation, angiogenesis, for treating solid tumours, chronic
 CC infections, leukaemia, T-cell mediated autoimmune diseases, parasitic
 CC infections, psoriasis and for stimulating growth factor activity. The
 CC compounds are also useful for treating allergy, anaphylaxis,
 CC atherogenesis, malignancy, chronic and acute inflammation, histamine and
 CC IgE-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and
 CC hyper-eosinophilic syndrome. The present sequence is a human MCP-1
 CC receptor protein. This sequence is used in the invention.
 XX
 SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.4e-198;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	344

RESULT 12

AAB46859

ID AAB46859 standard; protein; 329 AA.

XX

AC AAB46859;

XX

DT 16-AUG-2001 (revised)

DT 02-AUG-2001 (revised)

DT 04-MAY-2001 (first entry)

XX

DE Human MCP-1 receptor protein fragment.

XX

KW HDG NR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulnerary.

XX

OS Homo sapiens.

XX

PN US2001000241-A1.

XX

PD 12-APR-2001.

XX

PF 29-NOV-2000; 2000US-00725285.

XX

PR 06-JUN-1995; 95US-00466343.

PR 18-NOV-1998; 98US-00195662.

PR 25-JUN-1999; 99US-00339912.

XX

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2001-226317/23.

XX

PT New human G-protein chemokine receptor polypeptides and polynucleotides,
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.

XX

PS Disclosure; Page 16-17; 22pp; English.

XX

CC This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
CC products of the invention have antiinflammatory, immunomodulatory,
CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
CC activity and can be used for gene therapy. The G-protein chemokine
CC receptors, HDGMR10, (I) are useful for screening for compounds which
CC activate or inhibit activation of (I). The products of the invention can
CC also be used for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
CC stimulating growth factor activity. HDGMR10 is useful for treating
CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
CC reactions, prostaglandin-independent fever, bone marrow failure,
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
CC errors in the keyword formatting)

XX

SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 4; Length 329;

Best Local Similarity 95.6%; Pred. No. 1.7e-187;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          ||||||||||||||||||||||||||||||||||||||||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy     138 RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          ||||||||||||||||||||||||||||||||||||||||
Db     106 RYLAIVHAVFALKARTVTTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
          ||||||||||||||||||||||||||||||||||||||||
Db     166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225
```

QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
 |||
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285
 QY 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
 |||
 Db 286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

RESULT 13

ABB81055

ID ABB81055 standard; protein; 329 AA.

XX

AC ABB81055;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human MCP-1 receptor.

XX

KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;

KW G-protein chemokine receptor; haematopoietic; immunosuppressant;

KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;

KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.

XX

OS Homo sapiens.

XX

PN US2002076745-A1.

XX

PD 20-JUN-2002.

XX

PF 18-NOV-1998; 98US-00195662.

XX

PR 06-JUN-1995; 95US-00466343.

XX

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;

XX

DR WPI; 2002-598724/64.

XX

PT New polynucleotide encoding a human G protein chemokine receptor HDGNR10,

PT useful e.g. for treating tumors.

XX

PS Example; Fig 2; 22pp; English.

XX

CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,

CC which has been identified as a G-protein chemokine receptor. The GPCR

CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.

CC Compounds that activate or inhibit the receptor polypeptide, optionally

CC expressed from DNA in gene therapy vectors, are used to treat diseases

CC that require: (a) activation of the receptor (e.g. stimulation of

CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune

CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the

CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis

CC etc). The present sequence represents a human MCP-1 receptor used in

CC comparison studies with the HDGNR10 receptor

XX

SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 5; Length 329;
Best Local Similarity 95.6%; Pred. No. 1.7e-187;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy     138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy     318 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     286 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 14

AAR79166

ID AAR79166 standard; protein; 360 AA.

XX

AC AAR79166;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1. .48
FT		/label= extracellular
FT	Domain	49. .70
FT		/label= transmembrane
FT	Domain	80. .700
FT		/label= transmembrane
FT	Domain	115. .136
FT		/label= transmembrane

FT Domain 154. .178
 FT /label= transmembrane
 FT Domain 204. .231
 FT /label= transmembrane
 FT Domain 244. .268
 FT /label= transmembrane
 FT Domain 295. .313
 FT /label= transmembrane
 FT Region 314. .360
 FT /label= carboxyl tail
 XX
 PN WO9519436-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000476.
 XX
 PR 13-JAN-1994; 94US-00182962.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Charo I, Coughlin S;
 XX
 DR WPI; 1995-263866/34.
 DR N-PSDB; AAQ96298.
 XX
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX
 PS Claim 2; Fig 2; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pFROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 360 AA;

Query Match 83.8%; Score 1651.5; DB 2; Length 360;
 Best Local Similarity 95.5%; Pred. No. 8.6e-179;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```

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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
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Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334

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RESULT 15

AAW35833

ID AAW35833 standard; protein; 360 AA.

XX

AC AAW35833;

XX

DT 27-FEB-1998 (first entry)

XX

DE Human monocyte chemoattractant protein 1 receptor.

XX

KW Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;
 KW inflammatory disease; viral; allergy; diabetes.

XX

OS Homo sapiens.

XX

PN JP09238688-A.

XX

PD 16-SEP-1997.

XX

PF 11-MAR-1996; 96JP-00053574.

XX

PR 11-MAR-1996; 96JP-00053574.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

DR WPI; 1997-506557/47.

DR N-PSDB; AAT96976.

XX

PT DNA encoding human monocyte chemoattractant protein 1 receptor - used to
 PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and

PT central nervous system diseases.

XX

PS Disclosure; Page 12-14; 15pp; Japanese.

XX

CC The present sequence represents human monocyte chemoattractant protein 1
CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are
CC used for the prevention and treatment of tumours and inflammatory, viral,
CC infectious, allergic, diabetic and central nervous system diseases

XX

SQ Sequence 360 AA;

Query Match 83.8%; Score 1651.5; DB 2; Length 360;

Best Local Similarity 95.5%; Pred. No. 8.6e-179;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NP IIYAFVGEKFR---SLF---HIALG-CRIAPL 327
          |||  |||  |||  |||
Db    301 NP IIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334
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Search completed: January 10, 2005, 11:30:23

Job time : 159 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:39 ; Search time 39 Seconds
 (without alignments)
 635.973 Million cell updates/sec

Title: US-10-791-592-2
 Perfect score: 1970
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1970	100.0	374	1	US-08-450-393A-2	Sequence 2, Appli
2	1970	100.0	374	3	US-08-446-669-2	Sequence 2, Appli
3	1970	100.0	374	4	US-10-039-659A-14	Sequence 14, Appli
4	1970	100.0	374	4	US-09-625-573-2	Sequence 2, Appli
5	1970	100.0	374	5	PCT-US95-00476-2	Sequence 2, Appli
6	1823	92.5	344	3	US-08-466-343D-9	Sequence 9, Appli
7	1823	92.5	344	4	US-09-502-784A-9	Sequence 9, Appli
8	1727.5	87.7	329	4	US-09-502-783A-9	Sequence 9, Appli
9	1727.5	87.7	329	4	US-09-339-912A-9	Sequence 9, Appli
10	1651.5	83.8	360	1	US-08-450-393A-4	Sequence 4, Appli
11	1651.5	83.8	360	3	US-08-446-669-4	Sequence 4, Appli

12	1651.5	83.8	360	3	US-09-045-583-50	Sequence 50, Appl
13	1651.5	83.8	360	4	US-09-534-185-50	Sequence 50, Appl
14	1651.5	83.8	360	4	US-09-131-827A-2	Sequence 2, Appli
15	1651.5	83.8	360	4	US-09-625-573-4	Sequence 4, Appli
16	1651.5	83.8	360	5	PCT-US95-00476-4	Sequence 4, Appli
17	1650.5	83.8	360	4	US-09-131-827A-20	Sequence 20, Appl
18	1645.5	83.5	360	4	US-08-833-752-7	Sequence 7, Appli
19	1645.5	83.5	360	4	US-09-938-719-7	Sequence 7, Appli
20	1614.5	82.0	360	3	US-09-045-583-51	Sequence 51, Appl
21	1614.5	82.0	360	4	US-09-534-185-51	Sequence 51, Appl
22	1589.5	80.7	347	1	US-08-461-244-3	Sequence 3, Appli
23	1236	62.7	352	3	US-09-517-605-5	Sequence 5, Appli
24	1234	62.6	354	3	US-08-724-984A-2	Sequence 2, Appli
25	1230	62.4	352	3	US-09-045-583-52	Sequence 52, Appl
26	1230	62.4	352	4	US-09-534-185-52	Sequence 52, Appl
27	1224	62.1	352	3	US-09-087-232A-13	Sequence 13, Appl
28	1224	62.1	352	3	US-08-861-105-14	Sequence 14, Appl
29	1224	62.1	352	3	US-08-575-967A-2	Sequence 2, Appli
30	1224	62.1	352	4	US-08-833-752-5	Sequence 5, Appli
31	1224	62.1	352	4	US-09-502-783A-2	Sequence 2, Appli
32	1224	62.1	352	4	US-09-796-202-1	Sequence 1, Appli
33	1224	62.1	352	4	US-09-938-719-5	Sequence 5, Appli
34	1224	62.1	352	4	US-09-502-784A-2	Sequence 2, Appli
35	1224	62.1	352	4	US-09-339-912A-2	Sequence 2, Appli
36	1224	62.1	352	4	US-08-771-276-2	Sequence 2, Appli
37	1224	62.1	352	4	US-08-771-276-20	Sequence 20, Appl
38	1215	61.7	352	3	US-08-466-343D-2	Sequence 2, Appli
39	967.5	49.1	355	1	US-08-012-988A-2	Sequence 2, Appli
40	967.5	49.1	355	1	US-08-450-393A-5	Sequence 5, Appli
41	967.5	49.1	355	3	US-08-446-669-5	Sequence 5, Appli
42	967.5	49.1	355	3	US-09-239-938-1	Sequence 1, Appli
43	967.5	49.1	355	4	US-09-886-319A-14	Sequence 14, Appl
44	967.5	49.1	355	4	US-10-039-659A-13	Sequence 13, Appl
45	967.5	49.1	355	4	US-09-961-068-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-450-393A-2

; Sequence 2, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

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Query Match          100.0%; Score 1970; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
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Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
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Db    361 GRAPEASLQDKEGA 374

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RESULT 2

US-08-446-669-2

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; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
;   APPLICANT: Charo, Israel
;   APPLICANT: Coughlin, Shaun
;   TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;   TITLE OF INVENTION: PROTEIN RECEPTORS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;     STREET: 5 Palo Alto Square
;     CITY: Palo Alto
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94306-2155
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/446,669
;     FILING DATE: May 25, 1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Neeley, Richard
;     REGISTRATION NUMBER: 30,092
;     REFERENCE/DOCKET NUMBER: UCAL-237/01US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-843-5000
;     TELEFAX: 415-857-0663
;     TELEX: 380816CooleyPA
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 374 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
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US-08-446-669-2

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Query Match          100.0%; Score 1970; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFVGNAMCKLFTGLY 120
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Qy    121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db    121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
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 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

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 |||
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
 |||
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374
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 Db 361 GRAPEASLQDKEGA 374

RESULT 3

US-10-039-659A-14

; Sequence 14, Application US/10039659A
 ; Patent No. 6723520
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Wei
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Schall, Thomas J.
 ; APPLICANT: Vicari, Alain P.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Antibodies that bind chemokine TECK
 ; FILE REFERENCE: DX0589K1B US
 ; CURRENT APPLICATION NUMBER: US/10/039,659A
 ; CURRENT FILING DATE: 2002-01-03
 ; PRIOR APPLICATION NUMBER: US 08/887,977
 ; PRIOR FILING DATE: 1997-07-03
 ; PRIOR APPLICATION NUMBER: US 60/021,664
 ; PRIOR FILING DATE: 1996-07-05
 ; PRIOR APPLICATION NUMBER: US 60/028,329
 ; PRIOR FILING DATE: 1996-10-11
 ; PRIOR APPLICATION NUMBER: US 60/048,593
 ; PRIOR FILING DATE: 1997-06-04
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-039-659A-14

Query Match 100.0%; Score 1970; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.1e-150;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 |||
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120


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Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      361 GRAPEASLQDKEGA 374

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RESULT 4

US-09-625-573-2

; Sequence 2, Application US/09625573

; Patent No. 6730301

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/625,573

; FILING DATE: 25-Jul-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-625-573-2

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Query Match          100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
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Db    361 GRAPEASLQDKEGA 374

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RESULT 5

PCT-US95-00476-2

; Sequence 2, Application PC/TUS9500476

; GENERAL INFORMATION:

```

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor

```

```

;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90012-2628
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00476
;      FILING DATE:
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Berliner, Robert
;      REGISTRATION NUMBER:  20,121
;      REFERENCE/DOCKET NUMBER:  5555-291
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  310-977-1001
;      TELEFAX:  310-977-1003
;      TELEX:
;      INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
PCT-US95-00476-2

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Query Match          100.0%;  Score 1970;  DB 5;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 4.1e-150;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
|
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
|
Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|
Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|
Qy      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
|
Db      301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
|

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Qy      361 GRAPEASLQDKEG  374
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Db      361 GRAPEASLQDKEG  374

```

RESULT 6

US-08-466-343D-9

; Sequence 9, Application US/08466343D

; Patent No. 6025154

; GENERAL INFORMATION:

; APPLICANT: LI, Yi

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

```
; STATE: DC
```

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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;      COMPUTER:  IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/466,343D

; FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEO ID NO: 9:

; . SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

```
;      TYPE:  amino acid
```

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; STRANDEDNESS: single
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```
;      TOPOLOGY:  linear
```

```
; MOLECULE TYPE:  protein
```

US-08-466-343D-9

Query Match 92.5%; Score 1823; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.2e-138;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGNMLVVLILINCKKLKCLT 77

Db 1 EEVTTFFDYDYGAPCHKFDVKOIGAOLLPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

[illegible]

Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy	138	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180
Qy	198	WNNFHTIMRNILGLVLP	LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	181	WNNFHTIMRNILGLVLP	LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	240
Qy	258	PYNIVILLNTFQEFFGLSNCESTS	QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	241	PYNIVILLNTFQEFFGLSNCESTS	QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	300
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG		361
Db	301	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG		344

RESULT 7

US-09-502-784A-9

```

; Sequence 9, Application US/09502784A
; Patent No. 6743594
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
; TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
; FILE REFERENCE: 1488.1150005
; CURRENT APPLICATION NUMBER: US/09/502,784A
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-502-784A-9

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Query Match          92.5%; Score 1823; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-138;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	18	EEVTTFFDYDYGAPCHKFDVKQIGAQLLP	PLYSLVFIFGFVGNMLVVLILINCKKLKCLT	77
Db	1	EEVTTFFDYDYGAPCHKFDVKQIGAQLLP	PLYSLVFIFGFVGNMLVVLILINCKKLKCLT	60
Qy	78	DIYLLNLAISDLLFLITLPLWAHSAANEWV	FGNAMCKLFTGLYHIGYFGGIFFIILLTID	137
Db	61	DIYLLNLAISDLLFLITLPLWAHSAANEWV	FGNAMCKLFTGLYHIGYFGGIFFIILLTID	120
Qy	138	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	197
Db	121	RYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG	180

Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
 |||
 Db 181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240
 |||
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
 |||
 Db 241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
 |||
 Qy 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
 |||
 Db 301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
 |||

RESULT 8

US-09-502-783A-9

; Sequence 9, Application US/09502783A

; Patent No. 6511826

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)

; TITLE OF INVENTION: HDGNR10

; FILE REFERENCE: 1488.1150006

; CURRENT APPLICATION NUMBER: US/09/502,783A

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 9.1e-131;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
 |||
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
 |||
 Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
 |||
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105
 |||
 Qy 138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
 |||
 Db 106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165
 |||
 Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
 |||
 Db 166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 225
 |||

```

Qy      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          |||
Db      226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy      318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
          |||
Db      286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

```

RESULT 9

US-09-339-912A-9

```

; Sequence 9, Application US/09339912A
; Patent No. 6759519
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor
HDGNR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-339-912A-9

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Query Match      87.7%; Score 1727.5; DB 4; Length 329;
Best Local Similarity 95.6%; Pred. No. 9.1e-131;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

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Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
          |||
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
          |||
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy      138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          |||
Db      106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 257
          |||
Db      166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRVIFTIMIVYFLFWT 225

Qy      258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          |||
Db      226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

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Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120


```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      |||||||||||| |:| || | : |:
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPV 334

```

RESULT 11

US-08-446-669-4

; Sequence 4, Application US/08446669

; Patent No. 6132987

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match 83.8%; Score 1651.5; DB 3; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCCKQCPV 334
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RESULT 12

US-09-045-583-50

; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50

```

```

Query Match          83.8%; Score 1651.5; DB 3; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||
Db    301 NPIIYAFVGEKFRRLSVFFRKHITKRFCQCPV 334

```

RESULT 13

US-09-534-185-50

```

; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses

```

```

;                               Therefor
;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: LAHIVE & COCKFIELD, LLP
;       STREET: 28 State Street
;       CITY: Boston
;       STATE: Massachusetts
;       COUNTRY: USA
;       ZIP: 02109
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/534,185
;       FILING DATE: 24-Mar-2000
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 09/045,583
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Mandragouras, Amy E.
;       REGISTRATION NUMBER: 36,207
;       REFERENCE/DOCKET NUMBER: MNI-044
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617)227-7400
;       TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 50:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 360 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

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```

Query Match          83.8%;  Score 1651.5;  DB 4;  Length 360;
Best Local Similarity 95.5%;  Pred. No. 1.2e-124;
Matches 319;  Conservative 3;  Mismatches 5;  Indels 7;  Gaps 3;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

```

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Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
        |||
Db      301 NPIIYAFVGEKFRRLSVFFRKHITKRFCQCPV 334

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RESULT 14

US-09-131-827A-2

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; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

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Query Match      83.8%; Score 1651.5; DB 4; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.2e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

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Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFR---SLF---HIALG-CRIAPL	327
Db	301	NPIIYAFVGEKFRRLSVFFRKHITKRFCQCPV	334

Search completed: January 10, 2005, 11:34:25
Job time : 41 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:39 ; Search time 40 Seconds
 (without alignments)
 899.627 Million cell updates/sec

Title: US-10-791-592-2
 Perfect score: 1970
 Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	100.0	374	2	I38450	chemokine (C-C) re
2	1651.5	83.8	360	2	JC2443	chemokine (C-C) re
3	1224	62.1	352	2	A43113	chemokine (C-C) re
4	967.5	49.1	355	2	A45177	chemokine (C-C) re
5	960	48.7	359	2	I49341	MIP-1 alpha recept
6	902.5	45.8	355	2	I49339	macrophage inflamm
7	890.5	45.2	355	2	G02436	chemokine (C-C) re
8	833	42.3	360	2	JC4587	chemokine (C-C) re
9	831.5	42.2	360	2	A57160	chemokine (C-C) re
10	794.5	40.3	383	2	S55594	G protein-coupled
11	731	37.1	356	2	I49340	MIP-1 alpha recept
12	723	36.7	355	2	JC5067	G protein-coupled
13	704.5	35.8	354	2	I58186	probable G protein

14	698	35.4	355	2	JC4304	orphan G protein-c
15	644.5	32.7	344	2	JC5942	chemokine receptor
16	584	29.6	378	2	B55735	lymphocyte-specifi
17	575.5	29.2	378	2	A55735	G protein-coupled
18	570	28.9	378	2	A45680	G protein-coupled
19	554.5	28.1	369	2	JC5068	G protein-coupled
20	541.5	27.5	360	2	A53611	interleukin-8 rece
21	537	27.3	359	2	A48921	interleukin-8 rece
22	531	27.0	352	2	G00048	fusin (LESTRA) - c
23	530.5	26.9	353	2	S28787	neuropeptide Y/pep
24	529.5	26.9	355	2	JQ1231	interleukin-8 rece
25	528	26.8	352	2	A45747	neuropeptide Y/pep
26	526	26.7	358	2	A53752	interleukin-8 rece
27	526	26.7	367	2	JE0349	interferon-inducib
28	524.5	26.6	350	2	A39445	interleukin-8 rece
29	523	26.5	356	2	S42096	interleukin-8 rece
30	519	26.3	333	2	I65989	G protein-coupled
31	484	24.6	350	2	JN0621	G protein-coupled
32	480	24.4	359	2	A42656	angiotensin II rec
33	479.5	24.3	374	2	S42628	G protein-coupled
34	475	24.1	359	2	I51372	angiotensin II rec
35	473	24.0	359	2	JC2134	angiotensin II rec
36	472	24.0	359	2	JH0621	angiotensin II rec
37	471	23.9	359	2	S15403	angiotensin II rec
38	471	23.9	359	2	JQ1516	angiotensin II rec
39	469	23.8	359	2	JC1104	angiotensin II rec
40	468	23.8	359	2	S44425	angiotensin II rec
41	465	23.6	359	2	JC1194	angiotensin II rec
42	465	23.6	374	2	S32785	G protein-coupled
43	464	23.6	359	2	A48857	angiotensin II rec
44	461.5	23.4	372	2	S26667	G protein-coupled
45	460.5	23.4	327	2	S56162	MDCR15 protein - h

ALIGNMENTS

RESULT 1

I38450

chemokine (C-C) receptor 2, splice form A - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;
monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

C;Accession: I38450

* R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38450

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <RES>

A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;44-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;244-265/Domain: transmembrane #status predicted <TM6>

F;292-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          |||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          |||
Db    361 GRAPEASLQDKEGA 374
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RESULT 2

JC2443

chemokine (C-C) receptor 2, splice form B - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

* R; Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.

A;Reference number: JC2443; MUID:94324942; PMID:8048929

A;Accession: JC2443

A;Molecule type: mRNA

A;Residues: 1-360 <YAM>

A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-360 <RES>

A;Cross-references: EMBL:U03905; NID:q472557; PIDN:AAA19120.1; PID:q472558

C; Genetics:

A; Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;43-70/Domain: transmembrane #status predicted <TM1>

F;81-100/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>

F;244-268/Domain: transmembrane #status predicted <TM6>

F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;

Best Local Similarity 95.5%; Pred. No. 7.1e-137;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

[illegible]

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKOIGAOLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
| | | | |

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIGFFIIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

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Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db      241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      |||
Db      301 NPIIYAFVGEKFRRLSVFFRKHITKRCKQCPV 334

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RESULT 3

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor gene.

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.;

Saragosti, S.; Lapoumeroulie, C.; Cognaux, J.; Forceille, C.; Muyldermans, G.;

Verhofstede, C.; Burtonboy, G.; Georges, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth,

R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene.

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184, 'IKDSHLGAGPAAACHGHLLLGPNKNSASVSK' <SAM3>

A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection; it has an allele frequency of 0.09 or more in some caucasian populations and may have had a selective advantage by conferring resistance to Yersinia plague infections

R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1alpha, MIP-1beta, and RANTES.

A;Reference number: A58832; MUID:96295970; PMID:8699119
 A;Accession: A58832
 A;Molecule type: mRNA
 A;Residues: 1-352 <COM1>
 A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
 A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
 R;Combadiere, C.
 submitted to the EMBL Data Library, May 1996
 A;Reference number: H01541
 A;Accession: G02653
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-89,'L',91-352 <COM2>
 A;Cross-references: EMBL:U57840
 R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
 J. Biol. Chem. 271, 17161-17166, 1996
 A;Title: Molecular cloning and functional characterization of a novel human CC
 chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.
 A;Reference number: A58833; MUID:96291862; PMID:8663314
 A;Accession: A58833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
 C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-
 1beta (see PIR:A31767), and RANTES (see PIR:A28815).
 C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of
 chemokine (C-C) receptor 5 and T-cell surface glycoprotein CD4 (see PIR:RWHUT4).
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta
 and RANTES
 A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein;
 transmembrane protein
 F;32-56/Domain: transmembrane #status predicted <TM1>
 F;67-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/Disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;
 Best Local Similarity 76.3%; Pred. No. 1.8e-99;
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

Qy	24	FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
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Db	10	YDINYTTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL	69

Qy 82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA 141
 ||||| ||:| || | : | || | |:| ||| |:| ||||| |||||
 Db 70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIIFFIILLTIDRYLA 129

Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
 :|||:|||||:|||||:|||||: ||| | | :|| :
 Db 130 VHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHPYSQYQF 189

Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
 | || |: |||||:|||||:|||||:|||||:|||||:|||||
 Db 190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 249

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
 ||||:|||||:|| |::||| ||||| ||||| ||||| |||||
 Db 250 PYNIVLLLNTFQEFFGLNNCSSNRDLQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy 317 -----HIA 319
 |||
 Db 310 VFFQKHIA 317

RESULT 4

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A45177; I55671

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C;Genetics:

A;Gene: GDB:CMKBR1; CMKR-1

A;Cross-references: GDB:138446; OMIM:601159

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-264/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;
 Best Local Similarity 58.7%; Pred. No. 4.9e-77;
 Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

Qy	12	NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK	71
		: : : : : :	
Db	5	NTTED-YDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYK	63
Qy	72	KLKCLTDIYLLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIF	130
		: : : : : :	
Db	64	RLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYTGlySEIFF	123
Qy	131	IILLTIDRYLAIVHAVFALKARTVTFGVTVSVITWLVAVFASVPGIIFTKCQKEDSVYVC	190
		: : : : :	
Db	124	IILLTIDRYLAIVHAVFALRARTVTFGVITSIIWALAILASMPGLYFSKTQWEFTHHTC	183
Qy	191	GPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVAVRVIF	246
		: : : : : : :	
Db	184	SLHFPHESLREWKLQALKNLFGVLVPLLVMIICYTGIIKILLRRPNEKK-SKAVRLIF	242
Qy	247	TIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYA	306
		: : : : :	
Db	243	VIMIIFFLFWTPYNLILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYA	302
Qy	307	FVGEKF----RSLFH	317
		:	
Db	303	FVGERFRKYLRQLFH	317

RESULT 5

I49341

MIP-1 alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49341

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;
Best Local Similarity 50.1%; Pred. No. 2.2e-76;
Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

```
Qy      10 IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILIN 69
      |:  || |  || :|:: || |  :|::|: ||||| || | :||:|||||
Db      8 IKTVVESFE--TTPYEYEWAPPCEKVRikelGSWLLPPLYSLVFIIGLLGNMMVVLILIK 65

Qy      70 CKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
      :||: :|:| | ||||| || | | |  || | | : ||: :| |:: : |
Db      66 YRKLQIMTNIYLFNLAI SDLLFLFTVPFWIHVVLWNEWGFGHYMCKMLSGFYLLALYSEI 125

Qy     129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
      ||||| ||||| ||||| ||||| :||:| | :| |::| || : | :
Db     126 FFIILLTIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLALPEFIFHESQDSFGEF 185

Qy     189 VCGPYFPRG----WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRV 244
      | | :| |  | || : || || |||:|||||:||||| | ||:|:|:|
Db     186 SCSPRYPEGEEDSWKRFHALRMNIFGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRL 244

Qy     245 IFTIMIVYFLFWTPYPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPII 304
      || :||:|:| |||||:|:| : |  | :||: | | | ||| : |||:|:|
Db     245 IFVVMIVFFIFWTPYNLVLLFSAFHSTFLETSC EQSKHLDLAMQVTEVIAYTHCCVNPVI 304

Qy     305 YAFVGEKFRS----LFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGL---LDGRGKG 357
      |||||:| |  ||  :||: | : : | | | |
Db     305 YAFVGERFRKHLRLFFH-----RNVQFTWENIFQFLPGEENG 341

Qy     358 KSIGRAPEASLQD 370
      :: :|  |:
Db     342 RTSSVSPSTGEQE 354
```

RESULT 6

I49339

macrophage inflammatory protein-1 alpha receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49339

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49339

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <RES>

A;Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548

C;Superfamily: vertebrate rhodopsin

Query Match 45.8%; Score 902.5; DB 2; Length 355;
 Best Local Similarity 53.1%; Pred. No. 2.4e-71;
 Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;

```

Qy      21 TTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
      || |||  || | |: || ||||| ||| | |||:|:|:|: :|:|: ||
Db      13 TTEFDYGDSTPCQKTAVRAFGAGLLPPLYSLVFIIGVGNVLVILVLMQHRRLQSMTSIY 72

Qy      81 LLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRY 139
      | |||:|:|:| || | : :|:|:|:| ||| :| |:| : | ||||| |||
Db      73 LFNLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYFLGLYSEIFFIILLTIDRY 132

Qy     140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195
      |||||:|:| ||| |:|:|:| |:| |:| : | | | : | |:|
Db     133 LAIVHAVFALRARTVTLGIITSIIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL 192

Qy     196 RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLF 255
      : | | : |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     193 KQWKRFQALKLNLLGLILPLLVMIIICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLL 251

Qy     256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF--- 312
      ||||: : :|: : || : || | ||| : |||:|:| |||:|
Db     252 WTPYNLSVSVSAFQDVLFTNQCEQSKHLDLMAQVTEVIAYTHCCVNPPIIYFVGERFWKY 311

Qy     313 -RSLF--HIALGCRIAPLQK 329
      | || |:|: || |
Db     312 LRQLFQRHVAI-----PLAK 326

```

RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1, differs from the published sequence in having 281-Leu
 C;Genetics:
 A;Gene: GDB:CMKBR3
 A;Cross-references: GDB:579624; OMIM:601268
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 45.2%; Score 890.5; DB 2; Length 355;
 Best Local Similarity 54.6%; Pred. No. 2.7e-70;
 Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;

Qy	21	TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY	80
		::: : : : : ::: : :::	
Db	14	TSYYD-DVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVMILIKYRRRLRIMTNIY	72
Qy	81	LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY	139
		: : : : :	
Db	73	LLNLAISDLLFLVTLPLFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY	132
Qy	140	LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR---	196
		: : ::: : : : : : : :	
Db	133	LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV	192
Qy	197	-GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLF	255
		: : : : : : : :	
Db	193	YSWRHFHTLRMTIFCLVLP LLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF	251
Qy	256	WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-	314
		: : : : : : : : : : : : : : : :	
Db	252	WTPYNVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKY	311
Qy	315	---LFH	317
Db	312	LRHFFH	317

RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.3%; Score 833; DB 2; Length 360;
Best Local Similarity 47.9%; Pred. No. 2.9e-65;
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

```

Qy      10 IRNTNESGEEVTTFFDYD-YGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILI 68
      : : | :      : : : | :      | | | : | | | | | | | : | | | : | | : |
Db      6 VTDTTQDET VYNSYFYFESMPKPCTKEGIKAFGEVFLPPLYSLVFLGLFGNSVVVLVLF 65

Qy      69 NCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGI 128
      | : | | : | : | | | | | | | | : : | | : | : | | | : | : | : | |
Db      66 KYKRLKSMTDVYLLNLAISDLLFVLSLPFWGYAADQWVFGGLCKIVSWMYLVGFYSGI 125

Qy     129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
      | | | : : : | | | | | | | | | : | | : | : | | | | | | : | | :
Db     126 FFIMLSIDRYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHT 185

Qy     189 VCGPYF---PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRRAVRVI 245
      | :      |      : : | : | : : | | : | | | : : | | | : | | : |
Db     186 YCKTQYSVNSTTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLOHCKNEKK-NRAVRMI 244

Qy     246 FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIY 305
      | : : : : | | | | : | : | | | : | | | | | | | | | | | : | : |
Db     245 FGVVVLFLGFWTPYNVVLFLFETLVELEVLQDCTLERYLDYAIQATETLGFHCCCLNPVIY 304

Qy     306 AFVGEKFR----SLFHIALGCRIAPLQKPVCGGP 335
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     305 FFLGEKFRKYITQLFR-----TCRGP 325

```

RESULT 9

A57160

chemokine (C-C) receptor 4 - human

N;Alternate names: C-C CKR-4

C;Species: Homo sapiens (man)

C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
 J. Biol. Chem. 270, 19495-19500, 1995
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.
 A;Reference number: A57160; MUID:95370289; PMID:7642634
 A;Accession: A57160
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-360 <POW>
 A;Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
 A;Note: source clone K5-5
 C;Genetics:
 A;Gene: GDB:CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5; DB 2; Length 360;
 Best Local Similarity 51.9%; Pred. No. 3.9e-65;
 Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

Qy	31	PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL	90
		: : : : : :	
Db	28	PCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLL	87
Qy	91	FLITLPLWAHSAANEVVFNGAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALK	150
		: : : : : : : : : : : : :	
Db	88	FVFSLPFWGYAADQWVFGGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVHAVFSLR	147
Qy	151	ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---WNNFHTIMRN	207
		: : : : : : : : :	
Db	148	ARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTTWKVLSSLEIN	207
Qy	208	ILGLVLPPLLIMVICYSGILKTLRLCRNEKKRRAVRVIFTIMIVYFLFWTPYNIVILLNT	267
		: : : : : :	
Db	208	ILGLVIPLGIMLFCYSMIIRTQLQCKNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLET	266
Qy	268	FQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFHIALGCR	323

Db 267 LVELEVLQDCTFERYLDAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFKTCR 323

RESULT 10

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S55594

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 40.3%; Score 794.5; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 4 TSRSRFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61
| : : : : | | : | | | : | : | : | : | : | : | : | : | : | :
Db 32 TTIASLVPSTNSSDDYYDDLDDVDYEEAPCYKSDTTRLAAQVVPALYLLVFLFGLLGN 91
Qy 62 LVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 92 LVVIIVIRYMKIKNLTNMLLLNLAISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGV 151
Qy 120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFT 179
: : : : | | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 152 CYMSLYSQVFCIILLTVDRYLAVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFH 211
Qy 180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNE 235
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 212 GHQDDNGRVQCDPYPEMSTNVWRRRAHVAKVIMLSLILPLLIMAVCYVIIRLLR-RPS 270
Qy 236 KKRHRARVVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGM 295
| : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 271 KKKYKAIRLIFVIMVAYFVFWTPYNIVLLLSTFHATLLNLQCALSSNLDMALLITKTIVAY 330
Qy 296 THCCINPIIYAFVGEKFR---SLFHIALG---CRIAPLQKPVCGGPGVRPGKNVKVTTQ 348
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 331 THCCINPVIYAFVGEKFRRLHYHFFHTYVAIYLCKYIP----- 368
Qy 349 GLLDGRGKGK 358
| | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 369 -FLSGDGEGK 377

RESULT 11

I49340

MIP-1 alpha receptor like-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49340

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49340

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-356 <RES>

A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550

C;Superfamily: vertebrate rhodopsin

Query Match 37.1%; Score 731; DB 2; Length 356;
Best Local Similarity 46.6%; Pred. No. 2.4e-56;
Matches 137; Conservative 59; Mismatches 92; Indels 6; Gaps 3;

```
Qy      25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84
      | : | | : | : | | | | | | | : | : | | | : | | : | | | |
Db      18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy      85 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
      | | | | : | | | | : : | | | | | : | | : | : | | | | | | : |
Db      78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYFYLGLYSDFFITLLTIDRYLAVV 137

Qy     144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
      | | | | : | | | | | : | | | : | | | : | | | : | | |
Db     138 HVVFALRARTVTFGIISIIITWVLAALVSIPCLYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy     200 NFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWTPY 259
      | : | | | | : | | | : | | | : | | | : | | | : | | |
Db     198 RFQALTMNIGLILPLLAMIICYTRIINVLRH-RPNKKKAKVMRLIFVITLLFFLLAPY 256

Qy     260 NIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
      : : | : : : | : | : : | | | | | | : | | | : | |
Db     257 YLAAFVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFR 310
```

RESULT 12

JC5067

G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

A;Reference number: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 36.7%; Score 723; DB 2; Length 355;
Best Local Similarity 43.5%; Pred. No. 1.2e-55;
Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;

Qy	20	VTTFDYDY----	GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC	75
			: :: : : : : : :	
Db	9	VTTVTDYYPDIFSSPCDAELIQTNGKLLAVFYCLLFVFSLLGNSLVILVLVCKKLRS	68	
Qy	76	LTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLT	135	
		: : : : : : : : :	: : : : : : : : : :	
Db	69	ITDVYLLNLALSDLLFVFSFPFQTYLLDQWVFGTVMCKVVSGFYIIGFYSSMFITLMS	128	
Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195	
		: : : : : : : : :	: : : : : : :	
Db	129	VDRYLAVVHAVYALKVRTIRMGTTLC LAVWLTAIMATIPLLVFYQVASEDGVLCQCYSFYN	188	
Qy	196	R---GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRVAVRVIIFTIMIVY	252	
		: : : : : : : :		
Db	189	QOTLKWKIIFTNFKMNLGLLIPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLVIVIAS	247	
Qy	253	FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF	312	

```

      ||| |:|:| : | : | : || || ||| : ||||:|:| |||||
Db      248 LLFWVPFNVVLFSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAFVGEKF 307

Qy      313 R 313
      :
Db      308 K 308

```

RESULT 13

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: I58186

R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

A;Reference number: I58186; MUID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 35.8%; Score 704.5; DB 2; Length 354;

Best Local Similarity 47.6%; Pred. No. 5e-54;

Matches 151; Conservative 43; Mismatches 112; Indels 11; Gaps 6;

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Qy      24 FDYDYGA-PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL 82
      | :| | | | :| : | | | | | | | | | | | | | | | | | | | |
Db      13 FEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKSITSITDIYLL 72

Qy      83 NLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAI 142
      |||:||||: || | | : |||| | : ||:||||| :::|||
Db      73 NLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFFIGFFGGIFFITVISIDRYLAI 132

Qy      143 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRGWNNFH 202
      | | :| | | | | | : | | : | :| | :| :| | :|
Db      133 VLAANSMNRTVQHGVTTISLGVWAAAILVASPQFMFTK-RKDNE---CLGDYPEVLQEIW 188

Qy      203 TIMR---NILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLFWTP 258
      ::| ||| ||||| || |::| | :| || |::| :::|:|
Db      189 PVLNRSEVNILGFVLPLLIMSFYFRIVRTLFSCKNRKKA-RAIRLILLVVVVFFLEFWTP 247

Qy      259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFH 317
      |||| | | : : | | | | | | :||:| | | | | | | |
Db      248 YNIVIFLETLKFYNFFPSCGMKRDRLRWALSVTETVAFSHCLNPFIIYAFAGEKFRRYLRH 307

Qy      318 IALGCRIAPLQKPVC GG 334
      : | :| |
Db      308 LYNKCLAVLCGRPVHAG 324

```


RESULT 14

JC4304

orphan G protein-coupled receptor - human

N;Alternate names: V28 protein

C;Species: Homo sapiens (man)

C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C;Accession: JC4304

R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W. Gene 163, 295-299, 1995

A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neuraltissues.

A;Reference number: JC4304; MUID:96011651; PMID:7590284

A;Accession: JC4304

A;Molecule type: mRNA

A;Residues: 1-355 <RAP>

A;Cross-references: UNIPROT:P49238; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581

A;Experimental source: peripheral blood mononuclear cell

C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.

C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.

C;Genetics:

A;Gene: v28

A;Map position: 3pter-p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein

F;35-57/Domain: transmembrane #status predicted <TM1>

F;66-88/Domain: transmembrane #status predicted <TM2>

F;104-125/Domain: transmembrane #status predicted <TM3>

F;146-165/Domain: transmembrane #status predicted <TM4>

F;197-217/Domain: transmembrane #status predicted <TM5>

F;230-254/Domain: transmembrane #status predicted <TM6>

F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 35.4%; Score 698; DB 2; Length 355;

Best Local Similarity 45.3%; Pred. No. 1.9e-53;

Matches 146; Conservative 49; Mismatches 111; Indels 16; Gaps 7;

Qy	18	EEVTTFFDY-DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCL	76
		: : : : : :	
Db	6	ESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSV	65
Qy	77	TDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTI	136
		: : : : :	
Db	66	TDIYLLNLALSDDLFFVATLPFWTHYLINEKGLHNAMCKFTTAAFFFIGFFGSIFFITVISI	125
Qy	137	DRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR	196
		: : : : : :	
Db	126	DRYLAIVLAANSMMNRTVQHGVITISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE	181
Qy	197	GWNNFHTIMRNI----LGLVLP LLIMVICYSGILKTL LRCRNEKKRHRVAVRVI FTIMIVY	252
		: : : : : : : :	
Db	182	VLQEIWPVLRNVETNFLGFLLP LLIMSYCYFRIIQTLF SCKNHKKA-KAIKLILLVVIVF	240

Qy 253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312
 |||||:::| | : : :|: | | |||: :||:|:|||| ||||
 Db 241 FLFWTPYNVMIFLETCLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300
 Qy 313 RS-LFHIALGCRIAPLQKPVCVCG 333
 | |:|: | :||
 Db 301 RRYLYHLYGKCLAV-----LCG 317

RESULT 15

JC5942

chemokine receptor - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: JC5942

R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 243, 264-268, 1998

A;Title: Cloning and characterization of a novel human chemokine receptor.

A;Reference number: JC5942; MUID:98139902; PMID:9473515

A;Accession: JC5942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-344 <FAN>

A;Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:AAC39595.1;

PID:g2897071

C;Superfamily: vertebrate rhodopsin

Query Match 32.7%; Score 644.5; DB 2; Length 344;
 Best Local Similarity 39.9%; Pred. No. 8.7e-49;
 Matches 132; Conservative 58; Mismatches 120; Indels 21; Gaps 6;

Qy 27 DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAI 86
 | | |:| : : ||:| | | |: | : |:||||: | | : :|||||:
 Db 23 DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAV 82
 Qy 87 SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145
 |:| ||:| | |: | : ||: | | : | | ||: | | : |
 Db 83 SNLCFLLTLPFWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKG 136
 Qy 146 VFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCG----PYFPRG---W 198
 | | | |:| |: | : |: | : | | | | | | | : | | |
 Db 137 NFFSARRRVPCGIITSVLAWVTAILATLPEYVVYKQMEDQKYKCAFSRTPFLPADETFW 196
 Qy 199 NNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRVRVIFTIMIVYFLFWTP 258
 :| |: | | |||| | | : || | | : |: : :| |:|: | | |
 Db 197 KHFLT LKMNISVLVLP LFI FTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLMWAP 253
 Qy 259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS---- 314
 ||| |:| |:| | |:| |:| |:| :| : | | | | | :| | |
 Db 254 YNIAFFLSTFKEHFSLSDCSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTF SKYLCR 313
 Qy 315 LFHIALGCRIAPLQKPVCVCGGPGVRPGKNVKV 345
 |: | : | | | : |
 Db 314 CFHLRSNTPLQPRGQSAQGTSREEPDHSTEV 344

Search completed: January 10, 2005, 11:35:10

Job time : 41 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:33:45 ; Search time 750 Seconds
(without alignments)
179.805 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1970	100.0	374	10	US-09-893-512-13	Sequence 13, Appl
2	1970	100.0	374	14	US-10-039-659-14	Sequence 14, Appl
3	1970	100.0	374	14	US-10-239-423-63	Sequence 63, Appl
4	1970	100.0	374	16	US-10-754-071-14	Sequence 14, Appl
5	1970	100.0	374	16	US-10-741-601-287	Sequence 287, App
6	1970	100.0	374	17	US-10-791-592-2	Sequence 2, Appli
7	1970	100.0	374	17	US-10-791-166-2	Sequence 2, Appli
8	1823	92.5	344	9	US-09-779-879A-9	Sequence 9, Appli
9	1823	92.5	344	9	US-09-779-880A-9	Sequence 9, Appli
10	1823	92.5	344	14	US-10-232-686-9	Sequence 9, Appli
11	1823	92.5	344	14	US-10-067-800-9	Sequence 9, Appli
12	1823	92.5	344	14	US-10-135-839-9	Sequence 9, Appli
13	1727.5	87.7	329	9	US-09-725-285-9	Sequence 9, Appli
14	1727.5	87.7	329	9	US-09-195-662A-9	Sequence 9, Appli
15	1727.5	87.7	329	9	US-09-339-912A-9	Sequence 9, Appli
16	1727.5	87.7	329	9	US-09-502-783A-9	Sequence 9, Appli
17	1727.5	87.7	329	16	US-10-791-905-9	Sequence 9, Appli
18	1651.5	83.8	360	9	US-09-131-827A-2	Sequence 2, Appli
19	1651.5	83.8	360	14	US-10-225-567A-460	Sequence 460, App
20	1651.5	83.8	360	14	US-10-164-649-50	Sequence 50, Appl
21	1651.5	83.8	360	14	US-10-239-423-64	Sequence 64, Appl
22	1651.5	83.8	360	14	US-10-439-845-8	Sequence 8, Appli
23	1651.5	83.8	360	16	US-10-741-601-285	Sequence 285, App
24	1651.5	83.8	360	16	US-10-741-601-286	Sequence 286, App
25	1651.5	83.8	360	17	US-10-791-592-4	Sequence 4, Appli
26	1651.5	83.8	360	17	US-10-791-166-4	Sequence 4, Appli
27	1651.5	83.8	360	17	US-10-700-313-8	Sequence 8, Appli
28	1650.5	83.8	360	9	US-09-131-827A-20	Sequence 20, Appl
29	1645.5	83.5	360	9	US-09-938-719-7	Sequence 7, Appli
30	1645.5	83.5	360	9	US-09-939-226-7	Sequence 7, Appli
31	1645.5	83.5	360	9	US-09-938-703-7	Sequence 7, Appli
32	1645.5	83.5	360	10	US-09-826-509-473	Sequence 473, App
33	1645.5	83.5	360	16	US-10-661-798-7	Sequence 7, Appli
34	1645.5	83.5	360	16	US-10-612-791-7	Sequence 7, Appli
35	1614.5	82.0	360	14	US-10-164-649-51	Sequence 51, Appl
36	1589.5	80.7	347	9	US-09-104-792-3	Sequence 3, Appli
37	1589.5	80.7	347	14	US-10-176-078-3	Sequence 3, Appli
38	1589.5	80.7	347	17	US-10-893-996-3	Sequence 3, Appli
39	1582.5	80.3	384	10	US-09-893-512-14	Sequence 14, Appl
40	1236	62.7	352	14	US-10-151-274-5	Sequence 5, Appli
41	1230	62.4	352	14	US-10-164-649-52	Sequence 52, Appl
42	1224	62.1	352	9	US-09-725-285-2	Sequence 2, Appli
43	1224	62.1	352	9	US-09-759-841-2	Sequence 2, Appli
44	1224	62.1	352	9	US-09-779-879A-22	Sequence 22, Appl
45	1224	62.1	352	9	US-09-779-880A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-893-512-13

; Sequence 13, Application US/09893512

; Publication No. US20030017530A1

```

; GENERAL INFORMATION:
; APPLICANT: OWMAN, CHRISTER
; TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/893,512
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/061,789
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/081,958
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 09/170,069
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-512-13

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Query Match          100.0%; Score 1970; DB 10; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRLSFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        |||
Db    301 NPIIYAFVGEKFRLSFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        |||
Db    361 GRAPEASLQDKEGA 374

```

```

RESULT 2
US-10-039-659-14
; Sequence 14, Application US/10039659

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; Publication No. US20030018167A1
;   GENERAL INFORMATION:
;       APPLICANT: Wang, Wei
;               Gish, Kurt C.
;               Schall, Thomas J.
;               Vicari, Alain P.
;               Zlotnik, Albert
;   TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: DNAX Research Institute
;       STREET: 901 California Avenue
;       CITY: Palo Alto
;       STATE: California
;       COUNTRY: USA
;       ZIP: 94304-1104
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/039,659
;       FILING DATE: 03-Jan-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/887,977
;       FILING DATE: 03-JUL-1997
;       APPLICATION NUMBER: US 60/021,644
;       FILING DATE: 05-JUL-1996
;       APPLICATION NUMBER: US 60/028,329
;       FILING DATE: 11-OCT-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Ching, Edwin P.
;       REGISTRATION NUMBER: 34,090
;       REFERENCE/DOCKET NUMBER: DX0589K1
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 650-852-9192
;       TELEFAX: 650-496-1200
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 374 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14

```

```

Query Match          100.0%;  Score 1970;  DB 14;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 3.4e-163;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

```

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 |||
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 |||
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 |||
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
 |||
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy 361 GRAPEASLQDKEGA 374
 |||
 Db 361 GRAPEASLQDKEGA 374

RESULT 3

US-10-239-423-63

; Sequence 63, Application US/10239423

; Publication No. US20030186889A1

; GENERAL INFORMATION:

; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;

; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj

; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
 and

; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,

; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine

; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand

Interaction

; FILE REFERENCE: 022217us

; CURRENT APPLICATION NUMBER: US/10/239,423

; CURRENT FILING DATE: 2002-09-23

; PRIOR APPLICATION NUMBER: DE10016013.1

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies

US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;

Best Local Similarity 100.0%; Pred. No. 3.4e-163;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Db	301	NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI	360
Qy	361	GRAPEASLQDKEGA	374
Db	361	GRAPEASLQDKEGA	374

RESULT 4

US-10-754-071-14

; Sequence 14, Application US/10754071
 ; Publication No. US20040137578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Wei
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Schall, Thomas J.
 ; APPLICANT: Vicari, Alain P.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Chemokine TECK Polypeptides
 ; FILE REFERENCE: DX0589K1C US
 ; CURRENT APPLICATION NUMBER: US/10/754,071
 ; CURRENT FILING DATE: 2004-01-07
 ; PRIOR APPLICATION NUMBER: US 10/039,659
 ; PRIOR FILING DATE: 2002-01-03
 ; PRIOR APPLICATION NUMBER: US 08/887,977
 ; PRIOR FILING DATE: 1997-07-03
 ; PRIOR APPLICATION NUMBER: US 60/021,664
 ; PRIOR FILING DATE: 1996-07-05
 ; PRIOR APPLICATION NUMBER: US 60/028,329
 ; PRIOR FILING DATE: 1996-10-11
 ; PRIOR APPLICATION NUMBER: US 60/048,593
 ; PRIOR FILING DATE: 1997-06-04
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-754-071-14

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NP IIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NP IIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
          ||||||||||||
Db    361 GRAPEASLQDKEGA 374
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RESULT 5

US-10-741-601-287

; Sequence 287, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-287

Query Match 100.0%; Score 1970; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        |
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        |
Db    361 GRAPEASLQDKEGA 374

```

RESULT 6

US-10-791-592-2

; Sequence 2, Application US/10791592

; Publication No. US20040219644A1

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

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;      APPLICATION NUMBER: US/10/791,592
;      FILING DATE: 01-Mar-2004
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/625,573
;      FILING DATE: 25-Jul-2000
;      APPLICATION NUMBER: US/08/446,669
;      FILING DATE: May 25, 1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Neeley, Richard
;      REGISTRATION NUMBER: 30,092
;      REFERENCE/DOCKET NUMBER: UCAL-237/01US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 415-843-5000
;      TELEFAX: 415-857-0663
;      TELEX: 380816CooleyPA
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 374 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-592-2

```

```

Query Match          100.0%;  Score 1970;  DB 17;  Length 374;
Best Local Similarity 100.0%;  Pred. No. 3.4e-163;
Matches 374;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy    361 GRAPEASLQDKEGA 374
        ||||||||||||
Db    361 GRAPEASLQDKEGA 374

```

US-10-791-166-2

Query Match 100.0%; Score 1970; DB 17; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKOIGAQLLPPLYSLVFIFGFVGN 60

```

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy     181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db     181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy     241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db     241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy     301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
        |||
Db     301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy     361 GRAPEASLQDKEGA 374
        |||
Db     361 GRAPEASLQDKEGA 374

```

RESULT 8

US-09-779-879A-9

; Sequence 9, Application US/09779879A

; Patent No. US20020048786A1

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Roschke, Viktor

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDG NR10

; FILE REFERENCE: 1488.115000A

; CURRENT APPLICATION NUMBER: US/09/779,879A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 60/187,999

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/234,336

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 344

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-879A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;

Best Local Similarity 100.0%; Pred. No. 2e-150;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77

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Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120
Qy          138 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
Db          121 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
Qy          198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
Db          181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240
Qy          258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db          241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

```

RESULT 9

US-09-779-880A-9

; Sequence 9, Application US/09779880A

; Patent No. US20020061834A1

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Roschke, Viktor

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10

; FILE REFERENCE: 1488.115000C

; CURRENT APPLICATION NUMBER: US/09/779,880A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 60/187,999

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/234,336

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 344

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-880A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;

Best Local Similarity 100.0%; Pred. No. 2e-150;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77

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Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
 Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120
 Qy 138 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 RYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
 Qy 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240
 Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
 Qy 318 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 IALGCRIAPLQKPVC GPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

RESULT 10

US-10-232-686-9

; Sequence 9, Application US/10232686
 ; Publication No. US20030023044A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
 ; FILE REFERENCE: 1488.115000N
 ; CURRENT APPLICATION NUMBER: US/10/232,686
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: 09/339,912
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 09/195,662
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 08/466,343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-232-686-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-150;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
 Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137


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Db          |||||||||||||||||||||||||||||||||||||||||||||||||||||| 120
61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID

Qy          138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy          198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240

Qy          258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

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RESULT 11

US-10-067-800-9

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; Sequence 9, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-067-800-9

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Query Match          92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77

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Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 120
Qy          138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 197
Db          121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG 180
Qy          198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 257
Db          181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT 240
Qy          258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db          241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

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RESULT 12

US-10-135-839-9

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; Sequence 9, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDG NR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-9

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Query Match          92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77

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Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  60
Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
            |||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
Qy          138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
            |||
Db          121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180
Qy          198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVAVRVIFTIMIVYFLFWT 257
            |||
Db          181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVAVRVIFTIMIVYFLFWT 240
Qy          258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
            |||
Db          241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
Qy          318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
            |||
Db          301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344

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RESULT 13

US-09-725-285-9

; Sequence 9, Application US/09725285

; Patent No. US20010000241A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

; TITLE OF INVENTION: (CCR5 Receptor)

; FILE REFERENCE: 1488.1150003

; CURRENT APPLICATION NUMBER: US/09/725,285

; CURRENT FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 09/339,912

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-725-285-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

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Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  77
            |||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT  60

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Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
 ||||||||||||||||||||||||||||||||||||||||
 Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy 138 RYLAIHVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
 ||||||||||||||||||||||||||||||||||||||||
 Db 106 RYLAIHVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
 ||||||||||||||||||||||||||||||||||||||||
 Db 166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 225

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
 ||||||||||||||||||||||||||||||||||||||||
 Db 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy 318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
 ||||||||||||||||||||||||||||||||||||||||
 Db 286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

RESULT 14

US-09-195-662A-9

; Sequence 9, Application US/09195662A

; Patent No. US20020076745A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)

; FILE REFERENCE: 1488.1150002

; CURRENT APPLICATION NUMBER: US/09/195,662A

; CURRENT FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-195-662A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
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Db 1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTID 137
 ||||||||||||||||||||||||||||||||||||||||

Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

Qy 138 RYLAIHVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197

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Db      106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165
Qy      198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
Db      166 WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT 225
Qy      258 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
Db      226 PYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285
Qy      318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
Db      286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329

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RESULT 15

US-09-339-912A-9

; Sequence 9, Application US/09339912A

; Patent No. US20020099176A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDG NR10

; TITLE OF INVENTION: (CCR5 Receptor)

; FILE REFERENCE: 1488.1150003

; CURRENT APPLICATION NUMBER: US/09/339,912A

; CURRENT FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 329

; TYPE: PRT

; ORGANISM: Protein

US-09-339-912A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;

Best Local Similarity 95.6%; Pred. No. 3.9e-142;

Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

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Qy      18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKK LKCLT 77
Db      1  EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKK LKCLT 60
Qy      78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db      61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105
Qy      138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
Db      106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

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Qy	198	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
Db	166	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT	225
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	317
Db	226	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH	285
Qy	318	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	361
Db	286	IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG	329

Search completed: January 10, 2005, 11:57:29
Job time : 752 secs

OM protein - protein search, using sw model

Run on: January 10, 2005, 11:27:37 ; Search time 193 Seconds
(without alignments)
1114.975 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1970	100.0	374	1 CKR2_HUMAN	P41597 homo sapien
2	1614.5	82.0	360	1 CKR2_MACMU	O18793 macaca mula
3	1346.5	68.4	373	1 CKR2_RAT	O55193 rattus norv
4	1332.5	67.6	373	1 CKR2_MOUSE	P51683 mus musculu
5	1332.5	67.6	373	2 BAC32793	Bac32793 mus muscu
6	1327.5	67.4	373	2 Q6YT42	Q6yt42 sus scrofa
7	1327.5	67.4	373	2 BAD12134	Bad12134 sus scrof
8	1327.5	67.4	373	2 BAD08648	Bad08648 sus scrof
9	1327.5	67.4	373	2 BAD08655	Bad08655 sus scrof
10	1252	63.6	352	2 Q95NC2	Q95nc2 callicebus
11	1244	63.1	339	2 Q9TQT3	Q9tqt3 callithrix
12	1244	63.1	339	2 Q9TUV8	Q9tuv8 saguinus sp
13	1244	63.1	352	2 Q6WN98	Q6wn98 callithrix
14	1244	63.1	352	2 Q9MZA0	Q9mza0 callithrix
15	1244	63.1	352	2 AAQ20011	Aaq20011 callithri

16	1244	63.1	352	2	AAQ20012	Aaq20012 callithri
17	1244	63.1	352	2	AAQ20013	Aaq20013 callithri
18	1244	63.1	354	1	CKR5_MOUSE	P51682 mus musculu
19	1243	63.1	339	2	Q9TQV5	Q9tqv5 saguinus sp
20	1243	63.1	352	2	Q95NC4	Q95nc4 ateles geof
21	1241	63.0	352	2	Q6WN93	Q6wn93 leontopithe
22	1241	63.0	352	2	Q6WN96	Q6wn96 leontopithe
23	1241	63.0	352	2	Q6WN97	Q6wn97 cebuella py
24	1241	63.0	352	2	AAQ20014	Aaq20014 cebuella
25	1241	63.0	352	2	AAQ20015	Aaq20015 leontopit
26	1241	63.0	352	2	AAQ20018	Aaq20018 leontopit
27	1240	62.9	339	2	Q9TUW0	Q9tuw0 saguinus sp
28	1239	62.9	352	2	Q6YT41	Q6yt41 sus scrofa
29	1239	62.9	352	2	Q9MZ99	Q9mz99 ateles sp.
30	1239	62.9	352	2	BAD12135	Bad12135 sus scrof
31	1239	62.9	352	2	BAD08649	Bad08649 sus scrof
32	1239	62.9	352	2	BAD08656	Bad08656 sus scrof
33	1238.5	62.9	339	2	Q9TUV6	Q9tuv6 saguinus sp
34	1238	62.8	339	2	Q9TUW1	Q9tuw1 saguinus sp
35	1237	62.8	339	2	Q9TUV9	Q9tuv9 saguinus sp
36	1236	62.7	339	2	Q9TQW0	Q9tqw0 hylobates c
37	1236	62.7	352	1	CKR5_CERTO	O62743 cercocebus
38	1236	62.7	352	1	CKR5_HYLLE	O97883 hylobates l
39	1236	62.7	352	2	Q6WN92	Q6wn92 leontopithe
40	1236	62.7	352	2	Q6WN94	Q6wn94 leontopithe
41	1236	62.7	352	2	Q71RS2	Q71rs2 cercocebus
42	1236	62.7	352	2	Q8HZZ9	Q8hzt9 saimiri sci
43	1236	62.7	352	2	AAK69684	Aak69684 cercocebu
44	1236	62.7	352	2	AAQ20010	Aaq20010 saimiri s
45	1236	62.7	352	2	AAQ20017	Aaq20017 leontopit

ALIGNMENTS

RESULT 1

CKR2_HUMAN

ID CKR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN Name=CCR2; Synonyms=CMKBR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94324942; PubMed=8048929;
 RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
 RT "cDNA cloning and functional expression of a human monocyte
 RT chemoattractant protein 1 receptor."
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97150864; PubMed=8995400;
 RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
 RT "Organization and differential expression of the human monocyte
 RT chemoattractant protein 1 receptor gene. Evidence for the role of the
 RT carboxyl-terminal tail in receptor trafficking."
 RL J. Biol. Chem. 272:1038-1045(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
 RA Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
 RX MEDLINE=20501139; PubMed=11046064;
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
 RA Chakravarty L., Kolattukudy P.E.;
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
 RT has tyrosine sulfation in a conserved extracellular N-terminal
 RT region."
 RL J. Immunol. 165:5295-5303(2000).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=P41597-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P41597-2; Sequence=VSP_001893;
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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DR EMBL; U03882; AAA19119.1; -.
DR EMBL; U03905; AAA19120.1; -.
DR EMBL; D29984; BAA06253.1; -.
DR EMBL; U80924; AAC51637.1; -.
DR EMBL; U80924; AAC51636.1; -.
DR EMBL; U95626; AAB57791.1; -.
DR EMBL; U95626; AAB57792.1; -.
DR EMBL; AF545480; AAN16400.1; -.
DR PIR; I38450; I38450.
DR PIR; JC2443; JC2443.
DR PDB; 1KAD; Model; A=1-349.
DR PDB; 1KP1; Model; A=1-349.
DR Genew; HGNC:1603; CCR2.
DR MIM; 601267; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0004950; F:chemokine receptor activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
DR InterPro; IPR002237; CC_2_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW 3D-structure; Alternative splicing; G-protein coupled receptor;
KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.
FT DOMAIN 1 42 Extracellular (Potential).
FT TRANSMEM 43 70 1 (Potential).
FT DOMAIN 71 80 Cytoplasmic (Potential).
FT TRANSMEM 81 100 2 (Potential).
FT DOMAIN 101 114 Extracellular (Potential).
FT TRANSMEM 115 136 3 (Potential).
FT DOMAIN 137 153 Cytoplasmic (Potential).
FT TRANSMEM 154 178 4 (Potential).
FT DOMAIN 179 206 Extracellular (Potential).
FT TRANSMEM 207 226 5 (Potential).
FT DOMAIN 227 243 Cytoplasmic (Potential).
FT TRANSMEM 244 268 6 (Potential).
FT DOMAIN 269 285 Extracellular (Potential).
FT TRANSMEM 286 309 7 (Potential).
FT DOMAIN 310 374 Cytoplasmic (Potential).
FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
FT MOD_RES 26 26 Sulfotyrosine.
FT DISULFID 113 190 By similarity.

FT VARSPLIC 314 374 SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR
 FT GKKGKSGRAPEASLQDKEGA -> RYLSVFFRKHITKRFEK
 FT QCPVFYRETVDGVTSTNTPSTGEQEVSAAGL (in
 FT isoform B).
 FT /FTId=VSP_001893.
 FT VARIANT 64 64 V -> I (in dbSNP:1799864).
 FT /FTId=VAR_014339.
 FT VARIANT 355 355 G -> E.
 FT /FTId=VAR_014340.
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 100.0%; Score 1970; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.9e-120;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 Qy 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 Db 241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 2

CKR2_MACMU

ID CKR2_MACMU STANDARD; PRT; 360 AA.
 AC O18793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN Name=CCR2; Synonyms=CMKBR2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/088922201750290104;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF013958; AAD11572.1; -.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).
 FT TRANSMEM 207 226 5 (Potential).
 FT DOMAIN 227 243 Cytoplasmic (Potential).
 FT TRANSMEM 244 268 6 (Potential).
 FT DOMAIN 269 285 Extracellular (Potential).
 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 360 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT MOD_RES 26 26 Sulfotyrosine (By similarity).
 FT DISULFID 113 190 By similarity.

SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 82.0%; Score 1614.5; DB 1; Length 360;
Best Local Similarity 96.6%; Pred. No. 2.4e-97;
Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          ||:|||||
Db    181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||:|||||
Db    241 AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFR---SLF 316
          |||
Db    301 NPIIYAFVGEKFRRYLSMF 319
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RESULT 3

CKR2_RAT

ID CKR2_RAT STANDARD; PRT; 373 AA.
AC O55193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
GN Name=Ccr2; Synonyms=Cmkbr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

```
CC      -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC      macrophages.
CC      -!- INDUCTION: In animals in which experimental allergic
CC      encephalomyelitis (EAE) has been induced.
CC      -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
```

```

CC      EMBL; U77349; AAC03242.1; -.
DR      RGD; 620876; Ccr2.
DR      InterPro; IPR002237; CC_2_receptor.
DR      InterPro; IPR000355; Chmkine_receptor.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane.
FT      DOMAIN          1          60          Extracellular (Potential).
FT      TRANSMEM        61          81          Potential.
FT      DOMAIN          82          91          Cytoplasmic (Potential).
FT      TRANSMEM        92         112          Potential.
FT      DOMAIN         113         128          Extracellular (Potential).
FT      TRANSMEM        129         149          Potential.
FT      DOMAIN         150         170          Cytoplasmic (Potential).
FT      TRANSMEM        171         191          Potential.
FT      DOMAIN         192         220          Extracellular (Potential).
FT      TRANSMEM        221         241          Potential.
FT      DOMAIN         242         256          Cytoplasmic (Potential).
FT      TRANSMEM        257         277          Potential.
FT      DOMAIN         278         301          Extracellular (Potential).
FT      TRANSMEM        302         322          Potential.
FT      DOMAIN         323         373          Cytoplasmic (Potential).
FT      DISULFID        126         203          By similarity.
SQ      SEQUENCE      373 AA;  42763 MW;  2E7BB012F5D6FD09 CRC64;

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Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
		: : : :	
Db	14	ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN	73
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
		:: : : :	
Db	74	MLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGLY	133
Qy	121	HIGYFGGIIFFIILLTDIRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
		: : : : : : : :	
Db	134	HIGYFGGIIFFIILLTDIRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK	193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
 Db 194 SEQEDDQHTCGPYFPTIWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRRCRNEKKRHR 253
 Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 Db 254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQEFLGMSNCVVDMLDQAMQVTETLGMTHCCV 313
 Qy 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
 Db 314 NPIIYAFVGEKFRRLYSIFFRKHIAKNLCKQCPV 347

RESULT 4

CKR2_MOUSE

ID CKR2_MOUSE STANDARD; PRT; 373 AA.
 AC P51683; Q61172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 DE (JE/FIC receptor) (MCP-1 receptor).
 GN Name=Ccr2; Synonyms=Cmkbr2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gosling J., Montecarlo F.S., Lusic A.J., Tsou C.-L.,
 RA Charo I.F.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=96216064; PubMed=8662823;
 RA Kurihara T., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for the
 RT C-C chemokines JE and FIC.";
 RL J. Biol. Chem. 271:11603-11606(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97026720; PubMed=8872898;
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
 RT transcriptase-polymerase chain reaction does not detect mRNA for the
 RT KC or new MCP-1 receptor.";
 RL J. Neurosci. Res. 45:382-391(1996).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular

CC calcium ions level.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

DR EMBL; U47035; AAC52453.1; -.

DR EMBL; U51717; AAC52557.1; -.

DR EMBL; U56819; AAC52784.1; -.

DR MGD; MGI:106185; Ccr2.

DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

DR GO; GO:0019955; F:cytokine binding; IPI.

DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.

DR GO; GO:0030097; P:hemopoiesis; IMP.

DR GO; GO:0006959; P:humoral immune response; IMP.

DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0019233; P:perception of pain; IMP.

DR GO; GO:0030334; P:regulation of cell migration; IMP.

DR InterPro; IPR002237; CC_2_receptor.

DR InterPro; IPR000355; Chmkine_receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT	DOMAIN	1	55	Extracellular (Potential).
FT	TRANSMEM	56	83	1 (Potential).
FT	DOMAIN	84	93	Cytoplasmic (Potential).
FT	TRANSMEM	94	114	2 (Potential).
FT	DOMAIN	115	127	Extracellular (Potential).
FT	TRANSMEM	128	149	3 (Potential).
FT	DOMAIN	150	166	Cytoplasmic (Potential).
FT	TRANSMEM	167	191	4 (Potential).
FT	DOMAIN	192	219	Extracellular (Potential).
FT	TRANSMEM	220	239	5 (Potential).
FT	DOMAIN	240	256	Cytoplasmic (Potential).
FT	TRANSMEM	257	281	6 (Potential).
FT	DOMAIN	282	298	Extracellular (Potential).
FT	TRANSMEM	299	322	7 (Potential).
FT	DOMAIN	323	373	Cytoplasmic (Potential).
FT	DISULFID	126	203	By similarity.
FT	CONFLICT	39	39	Y -> H (in Ref. 1).
FT	CONFLICT	184	184	A -> G (in Ref. 1).
FT	CONFLICT	264	264	V -> G (in Ref. 1).
SQ	SEQUENCE	373 AA;	42782 MW;	FA012C10F4C9325A CRC64;

Query Match 67.6%; Score 1332.5; DB 1; Length 373;
Best Local Similarity 76.3%; Pred. No. 5.5e-79;

Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :||| | | : | | || :|| | ||| ||||| :|||||
Db      14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||:| | |||| :||||| ||| ||| ||||| |||:| |
Db      74 MLVILILIGCKKLKSMTDIYLLNLAISDLLFLITLPLFWAHYAANEWVFGNIMCKVFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
      ::| | |||| : | | ||||| :|||:| ||||| || |||||
Db    194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLLMVICYSGILHTLFCRNEKKRHR 253

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||:| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDQAMQVTETLGMTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
      ||:||||||| | :| ||| | : | :
Db    314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPV 347

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RESULT 5

BAC32793

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ID   BAC32793     PRELIMINARY;          PRT;   373 AA.
AC   BAC32793;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   4 days neonate male adipose cDNA, RIKEN full-length enriched library,
DE   clone:B430108F19 product:chemokine (C-C) receptor 2, full insert
DE   sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Adipose;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Adipose;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).

```

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK046579; BAC32793.1; -.
 KW Receptor.
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 67.6%; Score 1332.5; DB 2; Length 373;
 Best Local Similarity 76.3%; Pred. No. 5.5e-79;
 Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 :||||| | | : | | || :||| | |||| ||||| :|||||||
 Db 14 ILSTSHSLFTRSIQELDEGATTPYDYGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy 61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 |||::||| ||||| :|||||||:|||| ||| ||||| |||:|||||
 Db 74 MLVILIGCKKLSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 :::| | ||||| : | | ||||| |:||||:||||||| | | |||||
 Db 194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLVMVICYSGILHTLFRNEKKRHR 253

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||:|| |||||:| |||| |:||| ||| |||||
 Db 254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDDQAMQVTETLGMTHCCI 313

Qy 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
 ||:||||||| |:| ||| |: |:|
 Db 314 NPVIYAFVGEKFRRYLSIFFRKHIKRLCKQCPV 347

RESULT 6

Q6YT42

ID Q6YT42 PRELIMINARY; PRT; 373 AA.
 AC Q6YT42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
 DE 2).
 GN Name=CCR2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 RA Uenishi H.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP006185; BAD08648.1; -.
 DR EMBL; AP006435; BAD08655.1; -.
 DR EMBL; AB119271; BAD12134.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.

DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;
 Best Local Similarity 76.0%; Pred. No. 1.2e-78;
 Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          :| || |   |   : || || :||| || | | || | ||||| ||||| |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
          :||| ||||| ||| :||| ||||| ||| :| || ||| :||| || |||||
Db     74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||: ||: ||: ||| :
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
          |:| | | | ||| | ||||| :||| ||||| :||: ||||| ||||| ||| :|:
Db    194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTL LRCRNEKKKHK 253

Qy    241 AVRVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
          |||: || ||||| ||||| :||: || ||||| :||: ||||| ||||| :||| |
Db    254 AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
          ||||| ||||| |:| ||| |: |:
Db    314 NPIIYAFVGEKFRRYLSVFFRKHI AKHLCKQCPV 347

```

RESULT 7

BAD12134

ID BAD12134 PRELIMINARY; PRT; 373 AA.
 AC BAD12134;
 DT 03-MAR-2004 (TrEMBLrel. 27, Created)
 DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine C-C motif receptor 2.
 GN CCR2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 RA Uenishi H.;
 RT "Analysis of genomic structure of porcine CC chemokine receptor genes
 RT and their expression."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB119271; BAD12134.1; -.

KW Receptor.

SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;
Best Local Similarity 76.0%; Pred. No. 1.2e-78;
Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          :| || |   |   : || || :||| || | | || | ||||| ||||| |||||
Db      14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          :||| ||||| ||| :||| ||||| ||| :| || | ||: |||| || | ||||
Db     74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db    134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFIR 193

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHR 240
          |:| | | | |||| | ||||| :||| ||||| :||: ||||| ||||| ||||| :
Db    194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTL LRCRNEKKKHK 253

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||: || ||||| ||||| :||: ||| ||||| :||: ||||| ||||| :|||
Db    254 AVRLIFVIMIVYFLFWAPYNIVLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
          ||||| ||||| | :| ||| | : | :
Db    314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPV 347
```

RESULT 8

BAD08648

ID BAD08648 PRELIMINARY; PRT; 373 AA.
AC BAD08648;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2.
GN CCR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT "Cloning of porcine CC chemokine receptor genes and clustering
RT structure on SSC13.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006185; BAD08648.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 67.4%; Score 1327.5; DB 2; Length 373;
Best Local Similarity 76.0%; Pred. No. 1.2e-78;

Matches 254; Conservative 29; Mismatches 44; Indels 7; Gaps 3;

RESULT 9

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ID      BAD08655      PRELIMINARY;      PRT;      373 AA.
AC      BAD08655;
DT      02-MAR-2004 (TrEMBLrel. 27, Created)
DT      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT      02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE      Chemokine (C-C motif) receptor 2.
GN      CCR2.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT      "Cloning of porcine CC chemokine receptor genes and clustering
RT      structure on SSC13.";
RL      Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AP006435; BAD08655.1; -.
KW      Receptor.
SO      SEQUENCE      373 AA;  42299 MW;  FA8E55CA527A34E0 CRC64;
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Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGFVGN 60
 : | | | : | | | : ||| | | | | | | | | | | | | | |
Db 14 VLPTSHSLTMNIKGNDEEPTTSYDYDYSEPCOKTSGVQIEALLPPLYSLVFI FGFVGN 73

```

ID      Q95NC2                PRELIMINARY;          PRT;    352 AA.
AC      Q95NC2;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      C-C chemokine receptor 5.
GN      Name=CCR5;
OS      Callicebus moloch (Dusky titi).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC      Callicebus.
OX      NCBI_TaxID=9523;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang Y., Ryder O.A., Zhang Y.;
RL      Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR      EMBL; AF177887; AAK43370.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR      InterPro; IPR000923; BlueCu_1.
DR      InterPro; IPR002240; CC_5_receptor.
DR      InterPro; IPR000355; Chmkine_receptor.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00657; CCCHEMOKINER.
DR      PRINTS; PR01110; CHEMOKINER5.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00196; COPPER BLUE; UNKNOWN 1.

```

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 63.6%; Score 1252; DB 2; Length 352;
 Best Local Similarity 76.1%; Pred. No. 9e-74;
 Matches 239; Conservative 26; Mismatches 37; Indels 12; Gaps 3;

Qy 18 EEVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
 | : :| ||| | | | |||:|||||:|:|:|||||:|:|
 Db 4 EVSSPIYDIDYGASEPCQKIDVKQMGQAQLLPPLYSMVFLFGFVGNMLVVLILINCKRLKS 63

Qy 76 LTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLT 135
 :|||||:| | | | :| | | | :| | | | :| | | | |
 Db 64 MTDIYLLNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIIFIILLT 123

Qy 136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLAVFASVPGIIFTKQKEDSVYVCGPYFP 195
 |||||:|||||:|||||:|||||:| | | | | | | | |
 Db 124 IDRYLAIVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFP 183

Qy 196 RG----WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRVRVIFTIMIV 251
 | | | : | |||||:|||||:|||||:| | | | | | | | |
 Db 184 FGQYRFWKNLETLKMVILGLVLP LLVMVICYSGILKTL LRCRNEKKRHRVRRLIFTIMIV 243

Qy 252 YFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311
 |||| | ||||:||||:||||:| | | :::| | | | |||||:|||||
 Db 244 YFLFWAPYNIVLLNTYQEFFGLNNCSSNRDQAMQVTETLGMTHCCVNPIIYAFVGEK 303

Qy 312 FRSLF-----HIA 319
 ||: | |
 Db 304 FRNYLLVFFQKHIA 317

RESULT 11

Q9TQT3

ID Q9TQT3 PRELIMINARY; PRT; 339 AA.
 AC Q9TQT3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN Name=CCR5;
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22942991; PubMed=14581567;
 RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
 RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
 RA Doms R.W., Marx P., Wolinsky S.M.;
 RT "Structure and function of CC-chemokine receptor 5 homologues derived
 RT from representative primate species and subspecies of the taxonomic
 RT suborders Prosimii and Anthropoidea.";
 RL J. Virol. 77:12310-12318(2003).

RN [2]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF162021; AAD47776.1; -.
 DR EMBL; AF161934; AAD47691.1; -.
 DR EMBL; AF161935; AAD47692.1; -.
 DR EMBL; AF161936; AAD47693.1; -.
 DR EMBL; AF161937; AAD47694.1; -.
 DR EMBL; AF161938; AAD47695.1; -.
 DR EMBL; AF161939; AAD47696.1; -.
 DR EMBL; AF161940; AAD47697.1; -.
 DR EMBL; AF161944; AAD47700.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39055 MW; C1313952E71B50C7 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 339;
 Best Local Similarity 76.6%; Pred. No. 2.9e-73;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy 24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
 :| ||| || | ||||:| |||||:|:| ||||| |||||:| | ||||
 Db 3 YDIDYGPSEPCRKIDVKQMGHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 62

 Qy 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 |||||:| | :| ||| || :| ||| ||: ||| ||:| ||||| |||||
 Db 63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122

 Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
 ||||| ||||| |||||: |||||: |||||: ||| | | :| | :
 Db 123 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHPFQSQYQF 182

 Qy 198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
 | || |: |||||: ||||| ||||| |||||: ||||| |||||
 Db 183 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 242

Qy 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
 |||||:||||:|||||:| |::||| |||||:|||||:|||||:
 Db 243 PYNIVLLLNTYQEFFGLNNCSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA 302

Qy 317 -----HIA 319
 |||
 Db 303 VFFQKHIA 310

RESULT 12

Q9TUV8

ID Q9TUV8 PRELIMINARY; PRT; 339 AA.
 AC Q9TUV8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN Name=CCR5;
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22942991; PubMed=14581567;
 RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
 RA Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
 RA Doms R.W., Marx P., Wolinsky S.M.;
 RT "Structure and function of CC-chemokine receptor 5 homologues derived
 RT from representative primate species and subspecies of the taxonomic
 RT suborders Prosimii and Anthropoidea.";
 RL J. Virol. 77:12310-12318(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF161929; AAD47686.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000923; BlueCu_1...
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.

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FT    NON_TER      1      1
FT    NON_TER      339    339
SQ    SEQUENCE     339 AA; 39164 MW; 6A67CF5D22C70C49 CRC64;

Query Match          63.1%; Score 1244; DB 2; Length 339;
Best Local Similarity 77.3%; Pred. No. 2.9e-73;
Matches 238; Conservative 24; Mismatches 34; Indels 12; Gaps 3;

Qy      24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
      :| |||  || | ||||:| | |||||:|:| ||||| |||||: | :|||
Db      3 YDIDYGPSEPCRKIDVKQMGHLLPPLYSMVFLFGFVGNMLVVLILINCKRPKSMTDIYL 62

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      |||||:| | :| ||| || :| ||| ||: ||| ||:| ||||| |||||
Db      63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122

Qy     142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     123 IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSQKEGYHYTCSPHYFPGQYQF 182

Qy     198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRIFTIMIVYFLFWT 257
      | || |: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     183 WKNFETLKMVILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRVRLIFTIMIVYFLFWA 242

Qy     258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
      |||||:||||:|||||:| | |:| ||| ||||| ||||| ||||| ||||| :
Db     243 PYNIVLLLNTYQEFFGLNCSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLV 302

Qy     317 -----HIA 319
      |||
Db     303 VFFQKHIA 310

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RESULT 13

Q6WN98

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ID    Q6WN98      PRELIMINARY;      PRT;      352 AA.
AC    Q6WN98;
DT    05-JUL-2004 (TrEMBLrel. 27, Created)
DT    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT    05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE    CC chemokine receptor 5.
GN    Name=ccr5;
OS    Callithrix humeralifera (tassel-eared marmoset).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX    NCBI_TaxID=52232;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA    Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL    Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC    -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC    -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR    EMBL; AY278745; AAQ20013.1; -.
DR    EMBL; AY278744; AAQ20012.1; -.
DR    GO; GO:0004872; F:receptor activity; IEA.
DR    InterPro; IPR000923; BlueCu_1.

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DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40522 MW; FF0D0A852E553AF5 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3e-73;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy	24	FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL	81
		: : : : :	
Db	10	YDIDYGPSEPCRKIDVKQGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA	141
		: : : : :	
Db	70	LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG	197
		: : : : :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPFSQYQF	189
Qy	198	WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRRAVRVIFTIMIVYFLFWT	257
		: : :	
Db	190	WKNFETLKMVILGLVLPLLMVICYSGILKTLLRCRNEKKRHRRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF-	316
		: : : :	
Db	250	PYNIVLLLNTYQEFFGLNCSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLK	309
Qy	317	-----HIA	319
Db	310	VFFQKHIA	317

RESULT 14

Q9MZA0

ID Q9MZA0 PRELIMINARY; PRT; 352 AA.
 AC Q9MZA0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CC chemokine receptor 5 (Chemokine receptor CCR5).
 GN Name=CCR5; Synonyms=ccr5;
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20317091; PubMed=10747879;
 RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
 RA Begum K., Galvis M.C., Kostecky V., Valente A.J., Murthy K.K.,
 RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
 RT and mRNA. Potential roles for haplotype and mRNA diversity,
 RT differential haplotype-specific transcriptional activity, and altered
 RT transcription factor binding to polymorphic nucleotides in the
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
 RL J. Biol. Chem. 275:18946-18961(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22174698; PubMed=12186836;
 RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
 RT "Blockade of HIV-1 infection of New World monkey cells occurs
 RT primarily at the stage of virus entry.";
 RL J. Exp. Med. 196:431-445(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
 RA Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF252554; AAF87984.1; -.
 DR EMBL; AF452614; AAN14530.1; -.
 DR EMBL; AY278743; AAQ20011.1; -.
 DR EMBL; AF177878; AAK43361.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CICHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3e-73;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

Qy 24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
 :| ||| || | ||||:| | |||||:|:| ||||| |||||:| | :|||

Db	10	YDIDYGPSEPCRKIDVQKMGAAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL	69
Qy	82	LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLA	141
		: : : : :	
Db	70	LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFTGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP---RG	197
		: : : : :	
Db	130	IVHAVFALKARTVTFTGVVTSVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFPPFSQYQF	189
Qy	198	WNNFHTIMRNLGLVLP LLIMVICYS GILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT	257
		: : : : :	
Db	190	WKNFETLKMVILGLVLP LLVMVICYS GILKTL LRCRNEKKRHRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF-	316
		: : : : : :	
Db	250	PYNIVLLLNTYQEFFGLNNCSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA	309
Qy	317	-----HIA	319
Db	310	VFFOKHIA	317

RESULT 15

AAO20011

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ID      AAQ20011      PRELIMINARY;          PRT;    352 AA.
AC      AAQ20011;
DT      10-MAY-2004 (TrEMBLrel. 27, Created)
DT      10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT      10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE      CC chemokine receptor 5.
GN      CCR5.
OS      Callithrix jacchus (Common marmoset).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX      NCBI_TaxID=9483;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA      Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RT      "CCR5 chemokine receptor gene evolution in new world monkeys
RT      (Platyrrhini, Primates): implication on resistance to lentiviruses.";
RL      Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY278743; AAQ20011.1; -.
KW      Receptor.
SQ      SEQUENCE    352 AA;  40465 MW;  FF0D0A8D06F7B8F5 CRC64;

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Query Match 63.1%; Score 1244; DB 2; Length 352;
Best Local Similarity 76.6%; Pred. No. 3e-73;
Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

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Qy      24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKCLKLTDIYL 81
      :| ||| || | |||:| | |||||:| |:| ||||| |||||:| | :|||
Db      10 YDIDYGPSEPCRKIDVKQMGALLPPLYSMVFLFGFVGNMLVVLILINCKRCLKSMTDIYL 69

Qy      82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
      :| ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```

Db	70	LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA	129
Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFP----	RG 197
		: : : :	
Db	130	IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPPFSQYQF	189
Qy	198	WNNFHMTIMRNILGLVLPLLMVICYSYGILKTLLRCRNEKKRHRAVRVIIFTIMIVYFLFWT	257
		: : : : :	
Db	190	WKNFETLKMVILGLVLPLLVVICYSYGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA	249
Qy	258	PYNIVILLNTFQEFFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF-	316
		: : : : : : :	
Db	250	PYNIVLLLNTYQEFFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA	309
Qy	317	-----HIA	319
Db	310	VFFQKHIA	317

Search completed: January 10, 2005, 11:33:39
Job time : 195 secs